

#2



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/047,855

DATE: 02/05/2002

TIME: 16:19:33

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\02052002\J047855.raw

ENTERED

4 <110> APPLICANT: Chiang, Lillian Wei-Ming
6 <120> TITLE OF INVENTION: NARC10 and NARC16, Programmed Cell
7 Death-Associated Molecules and Uses Thereof
10 <130> FILE REFERENCE: 35800/242056
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/047,855
C--> 12 <141> CURRENT FILING DATE: 2002-01-15
12 <150> PRIOR APPLICATION NUMBER: US 60/262,306
13 <151> PRIOR FILING DATE: 2001-01-16
15 <160> NUMBER OF SEQ ID NOS: 16
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 182
21 <212> TYPE: PRT
22 <213> ORGANISM: Homo sapiens
24 <400> SEQUENCE: 1
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26 1 5 10 15
27 Ala Ala Ala Glu Ala Ala Ala Glu Glu Val Met Ala Glu Gly Gly Ala
28 20 25 30
29 Gln Gly Gly Asp Cys Asp Ser Ala Ala Gly Asp Pro Asp Ser Ala Ala
30 35 40 45
31 Gly Gln Met Ala Glu Glu Pro Gln Thr Pro Ala Glu Asn Ala Pro Lys
32 50 55 60
33 Pro Lys Asn Asp Phe Ile Glu Ser Leu Pro Asn Ser Val Lys Cys Arg
34 65 70 75 80
35 Val Leu Ala Leu Lys Lys Leu Gln Lys Arg Cys Asp Lys Ile Glu Ala
36 85 90 95
37 Lys Phe Asp Lys Glu Phe Gln Ala Leu Glu Lys Lys Tyr Asn Asp Ile
38 100 105 110
39 Tyr Lys Pro Leu Leu Ala Lys Ile Gln Glu Leu Thr Gly Glu Met Glu
40 115 120 125
41 Gly Cys Ala Trp Thr Leu Glu Gly Glu Glu Glu Glu Glu Glu Tyr
42 130 135 140
43 Glu Asp Asp Glu Glu Glu Gly Glu Asp Glu Glu Glu Glu Glu Ala Ala
44 145 150 155 160
45 Ala Glu Ala Ala Ala Gly Ala Lys His Asp Asp Ala His Ala Glu Met
46 165 170 175
47 Pro Asp Asp Ala Lys Lys
48 180
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 2034
53 <212> TYPE: DNA
54 <213> ORGANISM: Homo sapients

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56 <220> FEATURE:
57 <221> NAME/KEY: CDS
58 <222> LOCATION: (95)...(643)
60 <221> NAME/KEY: misc_feature
61 <222> LOCATION: (1)...(17)
62 <223> OTHER INFORMATION: vector sequence
64 <400> SEQUENCE: 2
65 gtcgacccac gcgtccggca agatctctct ggaccagctc ggggtgcaggg cctctgcggg 60
66 agccctccta gacctctgcg gcttctcttc taac atg gcc gac tcg gaa aac cag 115
67                                     Met Ala Asp Ser Glu Asn Gln
68                                     1           5
70 ggg cct gcg gag cct agc cag gcg gcg gca gcg gcg gag gca gcg gca 163
71 Gly Pro Ala Glu Pro Ser Gln Ala Ala Ala Ala Glu Ala Ala Ala
72      10           15           20
74 gag gag gta atg gcg gaa ggc ggt gcg cag ggt gga gac tgt gac agc 211
75 Glu Glu Val Met Ala Glu Gly Gly Ala Gln Gly Gly Asp Cys Asp Ser
76      25           30           35
78 gcg gct ggt gac cct gac agc gcg gct ggt cag atg gct gag gag ccc 259
79 Ala Ala Gly Asp Pro Asp Ser Ala Ala Gly Gln Met Ala Glu Glu Pro
80 40           45           50           55
82 cag acc cct gca gag aat gcc cca aag ccg aaa aat gac ttt atc gag 307
83 Gln Thr Pro Ala Glu Asn Ala Pro Lys Pro Lys Asn Asp Phe Ile Glu
84      60           65           70
86 agc ctg cct aat tcg gtg aaa tgc cga gtc ctg gcc ctc aaa aag ctg 355
87 Ser Leu Pro Asn Ser Val Lys Cys Arg Val Leu Ala Leu Lys Lys Leu
88      75           80           85
90 cag aag cga tgc gat aag ata gaa gcc aaa ttt gat aag gaa ttt cag 403
91 Gln Lys Arg Cys Asp Lys Ile Glu Ala Lys Phe Asp Lys Glu Phe Gln
92      90           95           100
94 gct ctg gaa aaa aag tat aat gac atc tat aag ccc cta ctc gcc aag 451
95 Ala Leu Glu Lys Lys Tyr Asn Asp Ile Tyr Lys Pro Leu Leu Ala Lys
96      105           110           115
98 atc caa gag ctc acc ggc gag atg gag ggg tgt gca tgg acc ttg gag 499
99 Ile Gln Glu Leu Thr Gly Glu Met Glu Gly Cys Ala Trp Thr Leu Glu
100 120           125           130           135
102 ggg gag gag gag gag gaa gag gag tac gag gat gac gag gag gag ggg 547
103 Gly Glu Glu Glu Glu Glu Glu Glu Tyr Glu Asp Asp Glu Glu Glu Gly
104      140           145           150
106 gaa gac gag gag gag gag gag gct gcg gca gag gct gcc gcg ggg gcc 595
107 Glu Asp Glu Glu Glu Glu Glu Ala Ala Ala Glu Ala Ala Ala Gly Ala
108      155           160           165
110 aaa cat gac gat gcc cac gcc gag atg cct gat gac gcc aag aag taa 643
111 Lys His Asp Asp Ala His Ala Glu Met Pro Asp Asp Ala Lys Lys *
112      170           175           180
114 ggggggcaga gatgatgaa gagaaagccc acgaagaaaa aagcctggtt ttgtttttcc 703
115 cagaatatcg atggacttaa aaaggctcag gtttttgacc aaaatacaat gtgaatttat 763
116 tctgacattc ctaaaataga tttaaattaaa gcaattagat cctggccagc tcgattcaaa 823
117 tttgactttc attttgaaca taataaatat atcaaaaggt gttaaagaaa actgaattaa 883
118 acccaaaatt atgttttcat ggtctcttct ctgaggattg aggtttacaa aggggtgttag 943

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119 cagatgcgaa gtaaagaacg tcactttgaa acccattcat cacacagcat acgctacaca 1003
120 tggaacacccc aagccatgac tgaacacggt ctcagtgtt aattcttaaa tttctttact 1063
121 catgacattt cgcagtgacg agaaggcaga acccaagaaa aacgtcatct ttgagacttt 1123
122 gcttttgtaa cgcagacatc agctttacac ttcacaggag attgatggca ttgaggaaga 1183
123 ttgcaatgga gatcatgaca ctactgttaa taaggccagg aaaactgcca tttcaagttc 1243
124 tgaaaaatgt tttgagtatt tgaatttaga gaaacaacat gggtccaaga aggagggtgt 1303
125 aaaacctgta aaatactgtc aacatatgta ttcattagtt acaatctcat gtttgtgttt 1363
126 tcttagtact gtctattttac aaacacgtaa aaaatacccc aaatatgttt aagtattaaa 1423
127 tcactttacc tagcgtttta gaaatattaa tttacttgaa gagatgtaga atgtagcaaa 1483
128 ttatgtaaag catgtgtatc cagcgttatg tactttgcgc cttgtgacgt ctttctgtca 1543
129 tgtagctttt aggggtgtagc tgtgaaaatc atcagaactc ttcactgaag ctaatgtttg 1603
130 gaaaaaatat atacttgaag aaccaatcca agtgtgtgcc cctaccccca gctcagaagt 1663
131 agaaagggtt taagtttgct tgtattagct gtgccttcat tattttgcta tgtaaagtgt 1723
132 acatattaat tataaatgg tgcataatca aattttactg cttgaggaca gatgcataca 1783
133 gtaaggattt ttaggaagaa tatatttaat gtaaagactc ttagcttctg tgtgggtttt 1843
134 gaattatgtg tgagccagtg atctataaag aaacataagc ttaaagttgt ttatcactgt 1903
135 ggtgttaata aaacagtatt ttcaaaaaat aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1963
136 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2023
137 agggcggccg c 2034

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139 <210> SEQ ID NO: 3

140 <211> LENGTH: 672

141 <212> TYPE: PRT

142 <213> ORGANISM: Homo sapiens

144 <400> SEQUENCE: 3

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145 Met Thr Pro Ser Gln Val Ala Phe Glu Ile Arg Gly Thr Leu Leu Pro
146 1 5 10 15
147 Gly Glu Val Phe Ala Ile Cys Gly Ser Cys Asp Ala Leu Gly Asn Trp
148 20 25 30
149 Asn Pro Gln Asn Ala Val Ala Leu Leu Pro Glu Asn Asp Thr Gly Glu
150 35 40 45
151 Ser Met Leu Trp Lys Ala Thr Ile Val Leu Ser Arg Gly Val Ser Val
152 50 55 60
153 Gln Tyr Arg Tyr Phe Lys Gly Tyr Phe Leu Glu Pro Lys Thr Ile Gly
154 65 70 75 80
155 Gly Pro Cys Gln Val Ile Val His Lys Trp Glu Thr His Leu Gln Pro
156 85 90 95
157 Arg Ser Ile Thr Pro Leu Glu Ser Glu Ile Ile Ile Asp Asp Gly Gln
158 100 105 110
159 Phe Gly Ile His Asn Gly Val Glu Thr Leu Asp Ser Gly Trp Leu Thr
160 115 120 125
161 Cys Gln Thr Glu Ile Arg Leu Arg Leu His Tyr Ser Glu Lys Pro Pro
162 130 135 140
163 Val Ser Ile Thr Lys Lys Lys Leu Lys Lys Ser Arg Phe Arg Val Lys
164 145 150 155 160
165 Leu Thr Leu Glu Gly Leu Glu Glu Asp Asp Asp Arg Val Ser Pro
166 165 170 175
167 Thr Val Leu His Lys Met Ser Asn Ser Leu Glu Ile Ser Leu Ile Ser
168 180 185 190
169 Asp Asn Glu Phe Lys Cys Arg His Ser Gln Pro Glu Cys Gly Tyr Gly

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170          195          200          205
171 Leu Gln Pro Asp Arg Trp Thr Glu Tyr Ser Ile Gln Thr Met Glu Pro
172          210          215          220
173 Asp Asn Leu Glu Leu Ile Phe Asp Phe Phe Glu Glu Asp Leu Ser Glu
174 225          230          235          240
175 His Val Val Gln Gly Asp Ala Leu Pro Gly His Val Gly Thr Ala Cys
176          245          250          255
177 Leu Leu Ser Ser Thr Ile Ala Glu Ser Gly Lys Ser Ala Gly Ile Leu
178          260          265          270
179 Thr Leu Pro Ile Met Ser Arg Asn Ser Arg Lys Thr Ile Gly Lys Val
180          275          280          285
181 Arg Val Asp Tyr Ile Ile Ile Lys Pro Leu Pro Gly Tyr Ser Cys Asp
182          290          295          300
183 Met Lys Ser Ser Phe Ser Lys Tyr Trp Lys Pro Arg Ile Pro Leu Asp
184 305          310          315          320
185 Val Gly His Arg Gly Ala Gly Asn Ser Thr Thr Thr Ala Gln Leu Ala
186          325          330          335
187 Lys Val Gln Glu Asn Thr Ile Ala Ser Leu Arg Asn Ala Ala Ser His
188          340          345          350
189 Gly Ala Ala Phe Val Glu Phe Asp Val His Leu Ser Lys Asp Phe Val
190          355          360          365
191 Pro Val Val Tyr His Asp Leu Thr Cys Cys Leu Thr Met Lys Lys Lys
192          370          375          380
193 Phe Asp Ala Asp Pro Val Glu Leu Phe Glu Ile Pro Val Lys Glu Leu
194 385          390          395          400
195 Thr Phe Asp Gln Leu Gln Leu Leu Lys Leu Thr His Val Thr Ala Leu
196          405          410          415
197 Lys Ser Lys Asp Arg Lys Glu Ser Val Val Gln Glu Glu Asn Ser Phe
198          420          425          430
199 Ser Glu Asn Gln Pro Phe Pro Ser Leu Lys Met Val Leu Glu Ser Leu
200          435          440          445
201 Pro Glu Asp Val Gly Phe Asn Ile Glu Ile Lys Trp Ile Cys Gln Gln
202          450          455          460
203 Arg Asp Gly Met Trp Asp Gly Asn Leu Ser Thr Tyr Phe Asp Met Asn
204 465          470          475          480
205 Leu Phe Leu Asp Ile Ile Leu Lys Thr Val Leu Glu Asn Ser Gly Lys
206          485          490          495
207 Arg Arg Ile Val Phe Ser Ser Phe Asp Ala Asp Ile Cys Thr Met Val
208          500          505          510
209 Arg Gln Lys Gln Asn Lys Tyr Pro Ile Leu Phe Leu Thr Gln Gly Lys
210          515          520          525
211 Ser Glu Ile Tyr Pro Glu Leu Met Asp Leu Arg Ser Arg Thr Thr Pro
212          530          535          540
213 Ile Ala Met Ser Phe Ala Gln Phe Glu Asn Leu Leu Gly Ile Asn Val
214 545          550          555          560
215 His Thr Glu Asp Leu Leu Arg Asn Pro Ser Tyr Ile Gln Glu Ala Lys
216          565          570          575
217 Ala Lys Gly Leu Val Ile Phe Cys Trp Gly Asp Asp Thr Asn Asp Pro
218          580          585          590

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219 Glu Asn Arg Arg Lys Leu Lys Glu Leu Gly Val Asn Gly Leu Ile Tyr
220          595          600          605
221 Asp Arg Ile Tyr Asp Trp Met Pro Glu Gln Pro Asn Ile Phe Gln Val
222          610          615          620
223 Glu Gln Leu Glu Arg Leu Lys Gln Glu Leu Pro Glu Leu Lys Ser Cys
224 625          630          635          640
225 Leu Cys Pro Thr Val Ser Arg Phe Val Pro Ser Ser Leu Cys Gly Glu
226          645          650          655
227 Ser Asp Ile His Val Asp Ala Asn Gly Ile Asp Asn Val Glu Asn Ala
228          660          665          670
231 <210> SEQ ID NO: 4
232 <211> LENGTH: 3206
233 <212> TYPE: DNA
234 <213> ORGANISM: Homo sapiens
236 <220> FEATURE:
237 <221> NAME/KEY: CDS
238 <222> LOCATION: (145)...(2163)
240 <221> NAME/KEY: misc_feature
241 <222> LOCATION: (1)...(17)
242 <223> OTHER INFORMATION: Vector sequence
244 <400> SEQUENCE: 4
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246 cctcgctctc gggcggggcg gcggcgacgc ggacctgcgg actagcgaac ccggagcacg 120
247 acatcataaa ataaatccat caga atg aca cct tct cag gtt gcc ttt gaa 171
248          Met Thr Pro Ser Gln Val Ala Phe Glu
249          1          5
251 ata aga gga act ctt tta cca gga gaa gtt ttt gcg ata tgt gga agc 219
252 Ile Arg Gly Thr Leu Leu Pro Gly Glu Val Phe Ala Ile Cys Gly Ser
253 10          15          20          25
255 tgt gat gct ttg gga aac tgg aat cct caa aat gct gtg gct ctt ctt 267
256 Cys Asp Ala Leu Gly Asn Trp Asn Pro Gln Asn Ala Val Ala Leu Leu
257          30          35          40
259 cca gag aat gac aca ggt gaa agc atg cta tgg aaa gca acc att gta 315
260 Pro Glu Asn Asp Thr Gly Glu Ser Met Leu Trp Lys Ala Thr Ile Val
261          45          50          55
263 ctc agt aga gga gta tca gtt cag tat cgc tac ttc aaa ggg tac ttt 363
264 Leu Ser Arg Gly Val Ser Val Gln Tyr Arg Tyr Phe Lys Gly Tyr Phe
265          60          65          70
267 tta gaa cca aag act atc ggt ggt cca tgt caa gtg ata gtt cac aag 411
268 Leu Glu Pro Lys Thr Ile Gly Gly Pro Cys Gln Val Ile Val His Lys
269          75          80          85
271 tgg gag act cat cta caa cca cga tca ata acc cct tta gaa agc gaa 459
272 Trp Glu Thr His Leu Gln Pro Arg Ser Ile Thr Pro Leu Glu Ser Glu
273 90          95          100          105
275 att att att gac gat gga caa ttt gga atc cac aat ggt gtt gaa act 507
276 Ile Ile Ile Asp Asp Gly Gln Phe Gly Ile His Asn Gly Val Glu Thr
277          110          115          120
279 ctg gat tct gga tgg ctg aca tgt cag act gaa ata aga tta cgt ttg 555
280 Leu Asp Ser Gly Trp Leu Thr Cys Gln Thr Glu Ile Arg Leu Arg Leu

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VERIFICATION SUMMARY

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DATE: 02/05/2002

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Input Set : A:\Seqlist.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date